

~~SEARCHED~~

## SEQUENCE LISTING

&lt;110&gt; John

&lt;120&gt; NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF

&lt;130&gt; 07334-340001

&lt;140&gt; 09/996,617

&lt;141&gt; 2001-11-27

&lt;150&gt; 09/931,071

&lt;151&gt; 2001-08-15

&lt;150&gt; 09/428,252

&lt;151&gt; 1999-10-27

&lt;150&gt; 09/340,620

&lt;151&gt; 1999-06-28

&lt;160&gt; 10

&lt;170&gt; FastSEQ for Windows Version 4.0

&lt;210&gt; 1

&lt;211&gt; 5444

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (523)...(4809)

&lt;400&gt; 1

gccccaggc	ctggagaggt	ctgaagaaac	ctgggagcca	gcagccggg	gctccactct	60
gggttctgaa	agcccatattcc	ctgtctcg	gctccatcca	ccccacacct	tctcagcc	120
gcagctcaag	ggttgcatttc	aggagtccag	gaccaggag	aggaaagaat	ctgaggaaca	180
cagaacagt	agcgttgccc	acacccatc	tcccgtaacc	acatctcccc	tcaccctcac	240
cctccctgcc	tggccctgga	ccccatccca	ggacccctt	atcagctgac	ttcttccagt	300
gtcttgcagg	cccctctggg	ctcctccctc	ccctggcttt	tccttaccact	ccccctctat	360
cggcgtctat	ctgttaggtgc	cctgggattt	ataaaactgg	gttccgaatg	ctgaataaga	420
gacggtaaga	gccaaggcaa	aggacagcac	tgttctctgc	ctgcctgata	ccctcaccac	480
ctgggaacat	cccccagaca	ccctcttaac	tccggacag	ag atg gct	ggc gga	534
				Met Ala Gly	Gly	
				1		

gcc tgg ggc cgc ctg gcc tgt tac ttg gag ttc	ctg aag aag gag gag	582
Ala Trp Gly Arg Leu Ala Cys Tyr Leu Glu Phe	Leu Lys Lys Glu Glu	
5	10	15
10	15	20

ctg aag gag ttc cag ctt ctg ctc gcc aat aaa	gcg cac tcc agg agc	630
Leu Lys Glu Phe Gln Leu Leu Ala Asn Lys Ala His	Ser Arg Ser	
25	30	35

tct tcg ggt gag aca ccc gct cag cca gag aag acg agt ggc atg gag		678
Ser Ser Gly Glu Thr Pro Ala Gln Pro Glu Lys Thr Ser Gly Met Glu		
40	45	50
gtg gcc tcg tac ctg gtg gct cag tat ggg gag cag cg <sup>g</sup> gcc tgg gac		726
Val Ala Ser Tyr Leu Val Ala Gln Tyr Gly Glu Gln Arg Ala Trp Asp		
55	60	65
cta gcc ctc cat acc tgg gag cag atg ggg ctg agg tca ctg tgc gcc		774
Leu Ala Leu His Thr Trp Glu Gln Met Gly Leu Arg Ser Leu Cys Ala		
70	75	80
caa gcc cag gaa ggg gca ggc cac tct ccc tca ttc ccc tac agc cca		822
Gln Ala Gln Glu Gly Ala Gly His Ser Pro Ser Phe Pro Tyr Ser Pro		
85	90	95
100		
agt gaa ccc cac ctg ggg tct ccc agc caa ccc acc tcc acc gca gtg		870
Ser Glu Pro His Leu Gly Ser Pro Ser Gln Pro Thr Ser Thr Ala Val		
105	110	115
cta atg ccc tgg atc cat gaa ttg ccg gc <sup>g</sup> ggg tgc acc cag ggc tca		918
Leu Met Pro Trp Ile His Glu Leu Pro Ala Gly Cys Thr Gln Gly Ser		
120	125	130
gag aga agg gtt ttg aga cag ctg cct gac aca tct gga cgc cgc tgg		966
Glu Arg Arg Val Leu Arg Gln Leu Pro Asp Thr Ser Gly Arg Arg Trp		
135	140	145
aga gaa atc tct gcc tca ctc ctc tac caa gct ctt cca agc tcc cca		1014
Arg Glu Ile Ser Ala Ser Leu Leu Tyr Gln Ala Leu Pro Ser Ser Pro		
150	155	160
gac cat gag tct cca agc cag gag tca ccc aac gcc ccc aca tcc aca		1062
Asp His Glu Ser Pro Ser Gln Glu Ser Pro Asn Ala Pro Thr Ser Thr		
165	170	175
180		
gca gtg ctg ggg agc tgg gga tcc cca cct cag ccc agc cta gca ccc		1110
Ala Val Leu Gly Ser Trp Gly Ser Pro Pro Gln Pro Ser Leu Ala Pro		
185	190	195
aga gag cag gag gct cct ggg acc caa tgg cct ctg gat gaa acg tca		1158
Arg Glu Gln Glu Ala Pro Gly Thr Gln Trp Pro Leu Asp Glu Thr Ser		
200	205	210
gga att tac tac aca gaa atc aga gaa aga gag aga gag aaa tca gag		1206
Gly Ile Tyr Tyr Thr Glu Ile Arg Glu Arg Glu Arg Glu Lys Ser Glu		
215	220	225
aaa ggc agg ccc cca tgg gca gc <sup>g</sup> gtg gta gga acg ccc cca cag gc <sup>g</sup>		1254
Lys Gly Arg Pro Pro Trp Ala Ala Val Val Gly Thr Pro Pro Gln Ala		
230	235	240
cac acc agc cta cag ccc cac cac cca tgg gag cct tct gtg aga		1302
His Thr Ser Leu Gln Pro His His Pro Trp Glu Pro Ser Val Arg		
245	250	255
260		

gag agc ctc tgt tcc aca tgg ccc tgg aaa aat gag gat ttt aac caa Glu Ser Leu Cys Ser Thr Trp Pro Trp Lys Asn Glu Asp Phe Asn Gln 265 270 275	1350
aaa ttc aca cag ctg cta ctt cta caa aga cct cac ccc aga agc caa Lys Phe Thr Gln Leu Leu Leu Gln Arg Pro His Pro Arg Ser Gln 280 285 290	1398
gat ccc ctg gtc aag aga agc tgg cct gat tat gtg gag gag aat cga Asp Pro Leu Val Lys Arg Ser Trp Pro Asp Tyr Val Glu Glu Asn Arg 295 300 305	1446
gga cat tta att gag atc aga gac tta ttt ggc cca ggc ctg gat acc Gly His Leu Ile Glu Ile Arg Asp Leu Phe Gly Pro Gly Leu Asp Thr 310 315 320	1494
caa gaa cct cgc ata gtc ata ctg cag ggg gct gct gga att ggg aag Gln Glu Pro Arg Ile Val Ile Leu Gln Gly Ala Ala Gly Ile Gly Lys 325 330 335 340	1542
tca aca ctg gcc agg cag gtg aag gaa gcc tgg ggg aga ggc cag ctg Ser Thr Leu Ala Arg Gln Val Lys Glu Ala Trp Gly Arg Gly Gln Leu 345 350 355	1590
tat ggg gac cgc ttc cag cat gtc ttc tac ttc agc tgc aga gag ctg Tyr Gly Asp Arg Phe Gln His Val Phe Tyr Phe Ser Cys Arg Glu Leu 360 365 370	1638
gcc cag tcc aag gtg gtg agt ctc gct gag ctc atc gga aaa gat ggg Ala Gln Ser Lys Val Val Ser Leu Ala Glu Leu Ile Gly Lys Asp Gly 375 380 385	1686
aca gcc act ccg gct ccc att aga cag atc ctg tct agg cca gag cgg Thr Ala Thr Pro Ala Pro Ile Arg Gln Ile Leu Ser Arg Pro Glu Arg 390 395 400	1734
ctg ctc ttc atc ctc gat ggt gta gat gag cca gga tgg gtc ttg cag Leu Leu Phe Ile Leu Asp Gly Val Asp Glu Pro Gly Trp Val Leu Gln 405 410 415 420	1782
gag ccg agt tct gag ctc tgt ctg cac tgg agc cag cca cag ccg gcg Glu Pro Ser Ser Glu Leu Cys Leu His Trp Ser Gln Pro Gln Pro Ala 425 430 435	1830
gat gca ctg ctg ggc agt ttg ctg ggg aaa act ata ctt ccc gag gca Asp Ala Leu Leu Gly Ser Leu Leu Gly Lys Thr Ile Leu Pro Glu Ala 440 445 450	1878
tcc ttc ctg atc acg gct cggt acc aca gct ctg cag aac ctc att cct Ser Phe Leu Ile Thr Ala Arg Thr Thr Ala Leu Gln Asn Leu Ile Pro 455 460 465	1926
tct ttg gag cag gca cgt tgg gta gag gtc ctg ggg ttc tct gag tcc Ser Leu Glu Gln Ala Arg Trp Val Glu Val Leu Gly Phe Ser Glu Ser 470 475 480	1974
agc agg aag gaa tat ttc tac aga tat ttc aca gat gaa agg caa gca	2022

Ser Arg Lys Glu Tyr Phe Tyr Arg Tyr Phe Thr Asp Glu Arg Gln Ala			
485	490	495	500
att aga gcc ttt agg ttg gtc aaa tca aac aaa gag ctc tgg gcc ctg			2070
Ile Arg Ala Phe Arg Leu Val Lys Ser Asn Lys Glu Leu Trp Ala Leu			
505	510	515	
tgt ctt gtg ccc tgg gtg tcc tgg ctg gcc tgc act tgc ctg atg cag			2118
Cys Leu Val Pro Trp Val Ser Trp Leu Ala Cys Thr Cys Leu Met Gln			
520	525	530	
cag atg aag cgg aag gaa aaa ctc aca ctg act tcc aag acc acc aca			2166
Gln Met Lys Arg Lys Glu Lys Leu Thr Leu Thr Ser Lys Thr Thr Thr			
535	540	545	
acc ctc tgt cta cat tac ctt gcc cag gct ctc caa gct cag cca ttg			2214
Thr Leu Cys Leu His Tyr Leu Ala Gln Ala Leu Gln Ala Gln Pro Leu			
550	555	560	
gga ccc cag ctc aga gac ctc tgc tct ctg gct gct gag ggc atc tgg			2262
Gly Pro Gln Leu Arg Asp Leu Cys Ser Leu Ala Ala Glu Gly Ile Trp			
565	570	575	580
caa aaa aag acc ctt ttc agt cca gat gac ctc agg aag cat ggg tta			2310
Gln Lys Lys Thr Leu Phe Ser Pro Asp Asp Leu Arg Lys His Gly Leu			
585	590	595	
gat ggg gcc atc atc tcc acc ttc ttg aag atg ggt att ctt caa gag			2358
Asp Gly Ala Ile Ile Ser Thr Phe Leu Lys Met Gly Ile Leu Gln Glu			
600	605	610	
cac ccc atc cct ctg agc tac agc ttc att cac ctc tgt ttc caa gag			2406
His Pro Ile Pro Leu Ser Tyr Ser Phe Ile His Leu Cys Phe Gln Glu			
615	620	625	
tcc ttt gca gca atg tcc tat gtc ttg gag gat gag aag ggg aga ggt			2454
Phe Phe Ala Ala Met Ser Tyr Val Leu Glu Asp Glu Lys Gly Arg Gly			
630	635	640	
aaa cat tct aat tgc atc ata gat ttg gaa aag acg cta gaa gca tat			2502
Lys His Ser Asn Cys Ile Ile Asp Leu Glu Lys Thr Leu Glu Ala Tyr			
645	650	655	660
gga ata cat ggc ctg ttt ggg gca tca acc aca cgt ttc cta ttg ggc			2550
Gly Ile His Gly Leu Phe Gly Ala Ser Thr Thr Arg Phe Leu Leu Gly			
665	670	675	
ctg tta agt gat gag ggg gag aga gag atg gag aac atc ttt cac tgc			2598
Leu Leu Ser Asp Glu Gly Glu Arg Glu Met Glu Asn Ile Phe His Cys			
680	685	690	
cgg ctg tct cag ggg agg aac ctg atg cag tgg gtc ccg tcc ctg cag			2646
Arg Leu Ser Gln Gly Arg Asn Leu Met Gln Trp Val Pro Ser Leu Gln			
695	700	705	
ctg ctg ctg cag cca cac tct ctg gag tcc ctc cac tgc ttg tac gag			2694
Leu Leu Leu Gln Pro His Ser Leu Glu Ser Leu His Cys Leu Tyr Glu			

710	715	720	
act	cg	a	2742
cgg	aa	aa	
a	ac	ac	
ttc	ctg	aca	
ca	aa	gt	
atg	gcc	at	
cat	tgc	gaa	
ttc	caa	gaa	
g	gt	gaa	
Th	Arg	Asn	
725	730	735	740
Met	Gly	Met	
745	750	755	
Cys	Val	Glu	
Met	Gly	Met	
755			
Thr	A	Sp	
760	765	770	
Phe	Ser	Arg	
Ile	Lys	Phe	
775	780	785	
His	Arg	Ser	
785			
Trp	Trp	Ser	
790	795	800	
Pro	Thr	Pro	
795	800		
Thr	Met	Val	
800			
Val	Val	Leu	
805			
Leu	Phe	Arg	
810			
Asn	Glu		
815			
Ser	Leu		
820			
Lys	Gly		
825			
Val	Asp		
830			
Ala	Tyr		
835			
Trp	Trp		
840			
Pro	Val		
845			
Val	Leu		
850			
Leu	Phe		
855			
Asp	Leu		
860			
Cys	Ala		
865			
Arg	Asn		
870			
Leu	Gln		
875			
Asp	Thr		
880			
Leu	Asp		
885			
Leu	Leu		
890			
Cys	Leu		
895			
Arg	Gln		
900			
Leu	Arg		
905			
Leu	Asp		
910			
Ser	Asp		
915			
Cys	Cys		
920			
Gly	Gly		
925			
Leu	Leu		
930			
Asp	Asp		
935			
Leu	Leu		
940			
Asp	Cys		
945			
Leu	Gly		
Arg	Leu		
His	Arg		

cct gcc tgc aaa ctc ata cgc ctg ggg ctg gac cag aca act ctg agt Pro Ala Cys Lys Leu Ile Arg Leu Gly Leu Asp Gln Thr Thr Leu Ser 950 955 960	3414
gat gag atg agg cag gaa ctg agg gcc ctg gag cag gag aaa cct cag Asp Glu Met Arg Gln Glu Leu Arg Ala Leu Glu Gln Glu Lys Pro Gln 965 970 975 980	3462
ctg ctc atc ttc agc aga cgg aaa cca agt gtg atg acc cct act gag Leu Leu Ile Phe Ser Arg Arg Lys Pro Ser Val Met Thr Pro Thr Glu 985 990 995	3510
ggc ctg gat acg gga gag atg agt aat agc aca tcc tca ctc aag cgg Gly Leu Asp Thr Gly Glu Met Ser Asn Ser Thr Ser Ser Leu Lys Arg 1000 1005 1010	3558
cag aga ctc gga tca gag agg gcg gct tcc cat gtt gct cag gct aat Gln Arg Leu Gly Ser Glu Arg Ala Ala Ser His Val Ala Gln Ala Asn 1015 1020 1025	3606
ctc aaa ctc ctg gac gtg agc aag atc ttc cca att gct gag att gca Leu Lys Leu Leu Asp Val Ser Lys Ile Phe Pro Ile Ala Glu Ile Ala 1030 1035 1040	3654
gag gaa agc tcc cca gag gta gta ccg gtg gaa ctc ttg tgc gtg cct Glu Glu Ser Ser Pro Glu Val Val Pro Val Glu Leu Leu Cys Val Pro 1045 1050 1055 1060	3702
tct cct gcc tct caa ggg gac ctg cat acg aag cct ttg ggg act gac Ser Pro Ala Ser Gln Gly Asp Leu His Thr Lys Pro Leu Gly Thr Asp 1065 1070 1075	3750
gat gac ttc tgg ggc ccc acg ggg cct gtg gct act gag gta gtt gac Asp Asp Phe Trp Gly Pro Thr Gly Pro Val Ala Thr Glu Val Val Asp 1080 1085 1090	3798
aaa gaa aag aac ttg tac cga gtt cac ttc cct gta gct ggc tcc tac Lys Glu Lys Asn Leu Tyr Arg Val His Phe Pro Val Ala Gly Ser Tyr 1095 1100 1105	3846
cgc tgg ccc aac acg ggt ctc tgc ttt gtg atg aga gaa gcg gtg acc Arg Trp Pro Asn Thr Gly Leu Cys Phe Val Met Arg Glu Ala Val Thr 1110 1115 1120	3894
gtt gag att gaa ttc tgt gtg tgg gac cag ttc ctg ggt gag atc aac Val Glu Ile Glu Phe Cys Val Trp Asp Gln Phe Leu Gly Glu Ile Asn 1125 1130 1135 1140	3942
cca cag cac agc tgg atg gtg gca ggg cct ctg gac atc aag gct Pro Gln His Ser Trp Met Val Ala Gly Pro Leu Leu Asp Ile Lys Ala 1145 1150 1155	3990
gag cct gga gct gtg gaa gct gtg cac ctc cct cac ttt gtg gct ctc Glu Pro Gly Ala Val Glu Ala Val His Leu Pro His Phe Val Ala Leu 1160 1165 1170	4038

caa ggg ggc cat gtg gac aca tcc ctg ttc caa atg gcc cac ttt aaa Gln Gly Gly His Val Asp Thr Ser Leu Phe Gln Met Ala His Phe Lys 1175 1180 1185	4086
gag gag ggg atg ctc ctg gag aag cca gcc agg gtg gag ctg cat cac Glu Glu Gly Met Leu Leu Glu Lys Pro Ala Arg Val Glu Leu His His 1190 1195 1200	4134
ata gtt ctg gaa aac ccc agc ttc tcc ccc ttg gga gtc ctc ctg aaa Ile Val Leu Glu Asn Pro Ser Phe Ser Pro Leu Gly Val Leu Leu Lys 1205 1210 1215 1220	4182
atg atc cat aat gcc ctg cgc ttc att ccc gtc acc tct gtg gtg ttg Met Ile His Asn Ala Leu Arg Phe Ile Pro Val Thr Ser Val Val Leu 1225 1230 1235	4230
ctt tac cac cgc gtc cat cct gag gaa gtc acc ttc cac ctc tac ctg Leu Tyr His Arg Val His Pro Glu Glu Val Thr Phe His Leu Tyr Leu 1240 1245 1250	4278
atc cca agt gac tgc tcc att cgg aag gaa ctg gag ctc tgc tat cga Ile Pro Ser Asp Cys Ser Ile Arg Lys Glu Leu Glu Leu Cys Tyr Arg 1255 1260 1265	4326
agc cct gga gaa gac cag ctg ttc tcg gag ttc tac gtt ggc cac ttg Ser Pro Gly Glu Asp Gln Leu Phe Ser Glu Phe Tyr Val Gly His Leu 1270 1275 1280	4374
gga tca ggg atc agg ctg caa gtg aaa gac aag aaa gat gag act ctg Gly Ser Gly Ile Arg Leu Gln Val Lys Asp Lys Lys Asp Glu Thr Leu 1285 1290 1295 1300	4422
gtg tgg gag gcc ttg gtg aaa cca gga gat ctc atg cct gca act act Val Trp Glu Ala Leu Val Lys Pro Gly Asp Leu Met Pro Ala Thr Thr 1305 1310 1315	4470
ctg atc cct cca gcc cgc ata gcc gta cct tca cct ctg gat gcc ccg Leu Ile Pro Pro Ala Arg Ile Ala Val Pro Ser Pro Leu Asp Ala Pro 1320 1325 1330	4518
cag ttg ctg cac ttt gtg gac cag tat cga gag cag ctg ata gcc cga Gln Leu Leu His Phe Val Asp Gln Tyr Arg Glu Gln Leu Ile Ala Arg 1335 1340 1345	4566
gtg aca tcg gtg gag gtt gtc ttg gac aaa ctg cat gga cag gtg ctg Val Thr Ser Val Glu Val Leu Asp Lys Leu His Gly Gln Val Leu 1350 1355 1360	4614
agc cag gag cag tac gag agg gtg ctg gct gag aac acg agg ccc agc Ser Gln Glu Gln Tyr Glu Arg Val Leu Ala Glu Asn Thr Arg Pro Ser 1365 1370 1375 1380	4662
cag atg cggtt aag ctg ttc agc ttg agc cag tcc tgg gac cgg aag tgc Gln Met Arg Lys Leu Phe Ser Leu Ser Gln Ser Trp Asp Arg Lys Cys 1385 1390 1395	4710
aaa gat gga ctc tac caa gcc ctg aag gag acc cat cct cac ctc att	4758

Lys Asp Gly Leu Tyr Gln Ala Leu Lys Glu Thr His Pro His Leu Ile			
1400	1405	1410	
atg gaa ctc tgg gag aag ggc agc aaa aag gga ctc ctg cca ctc agc			4806
Met Glu Leu Trp Glu Lys Gly Ser Lys Lys Gly Leu Leu Pro Leu Ser			
1415	1420	1425	
agc tgaagtatca acaccagccc ttgacccttg agtcctggct ttggctgacc			4859
Ser			
cttctttggg tctcaaggttc tttctctgca aacaagggtc catctggtt gccttccagc			4919
actaaagtaa tgaaaccttg atgatgcctt tgctggcat tatgtgtcca tgccaggat			4979
gccacagggg gccccagttc aggtggccta acagcatctc agggaatgtc catctggagc			5039
tggcaagacc cctcaagacc tcatacgagcc tcatactggtg gccacagcag ccaagcctag			5099
agccctccgg atcccatcca ggcgcaaaga ggaataggag ggacatggaa ccatttgcc			5159
ctggctgtgt cacagggtga gccccaaaat tggggttcag cgtggaggc cacgtggatt			5219
cttggctttt tacaggaaga tctacaagag caagccaaca gagtaaagt gaaggaagt			5279
tattcagaaa ataaaggagt atcacagctc ttttagaatt tgtcttagcag gctttccagt			5339
ttttaccaga aaaccctat aaattaaaaa tttttactt aaatttaaga attaaaaaaa			5399
tacaaaaaaag aaaaaatgaa aataaaggaa taagaagtta cctac			5444
<210> 2			
<211> 1429			
<212> PRT			
<213> Homo sapiens			
<400> 2			
Met Ala Gly Gly Ala Trp Gly Arg Leu Ala Cys Tyr Leu Glu Phe Leu			
1 5 10 15			
Lys Lys Glu Glu Leu Lys Glu Phe Gln Leu Leu Ala Asn Lys Ala			
20 25 30			
His Ser Arg Ser Ser Ser Gly Glu Thr Pro Ala Gln Pro Glu Lys Thr			
35 40 45			
Ser Gly Met Glu Val Ala Ser Tyr Leu Val Ala Gln Tyr Gly Glu Gln			
50 55 60			
Arg Ala Trp Asp Leu Ala Leu His Thr Trp Glu Gln Met Gly Leu Arg			
65 70 75 80			
Ser Leu Cys Ala Gln Ala Gln Glu Gly Ala Gly His Ser Pro Ser Phe			
85 90 95			
Pro Tyr Ser Pro Ser Glu Pro His Leu Gly Ser Pro Ser Gln Pro Thr			
100 105 110			
Ser Thr Ala Val Leu Met Pro Trp Ile His Glu Leu Pro Ala Gly Cys			
115 120 125			
Thr Gln Gly Ser Glu Arg Arg Val Leu Arg Gln Leu Pro Asp Thr Ser			
130 135 140			
Gly Arg Arg Trp Arg Glu Ile Ser Ala Ser Leu Leu Tyr Gln Ala Leu			
145 150 155 160			
Pro Ser Ser Pro Asp His Glu Ser Pro Ser Gln Glu Ser Pro Asn Ala			
165 170 175			
Pro Thr Ser Thr Ala Val Leu Gly Ser Trp Gly Ser Pro Pro Gln Pro			
180 185 190			
Ser Leu Ala Pro Arg Glu Gln Glu Ala Pro Gly Thr Gln Trp Pro Leu			
195 200 205			
Asp Glu Thr Ser Gly Ile Tyr Tyr Thr Glu Ile Arg Glu Arg Glu Arg			
210 215 220			
Glu Lys Ser Glu Lys Gly Arg Pro Pro Trp Ala Ala Val Val Gly Thr			

225	230	235	240
Pro Pro Gln Ala His Thr Ser Leu Gln Pro His His His Pro Trp Glu			
245	250	255	
Pro Ser Val Arg Glu Ser Leu Cys Ser Thr Trp Pro Trp Lys Asn Glu			
260	265	270	
Asp Phe Asn Gln Lys Phe Thr Gln Leu Leu Leu Leu Gln Arg Pro His			
275	280	285	
Pro Arg Ser Gln Asp Pro Leu Val Lys Arg Ser Trp Pro Asp Tyr Val			
290	295	300	
Glu Glu Asn Arg Gly His Leu Ile Glu Ile Arg Asp Leu Phe Gly Pro			
305	310	315	320
Gly Leu Asp Thr Gln Glu Pro Arg Ile Val Ile Leu Gln Gly Ala Ala			
325	330	335	
Gly Ile Gly Lys Ser Thr Leu Ala Arg Gln Val Lys Glu Ala Trp Gly			
340	345	350	
Arg Gly Gln Leu Tyr Gly Asp Arg Phe Gln His Val Phe Tyr Phe Ser			
355	360	365	
Cys Arg Glu Leu Ala Gln Ser Lys Val Val Ser Leu Ala Glu Leu Ile			
370	375	380	
Gly Lys Asp Gly Thr Ala Thr Pro Ala Pro Ile Arg Gln Ile Leu Ser			
385	390	395	400
Arg Pro Glu Arg Leu Leu Phe Ile Leu Asp Gly Val Asp Glu Pro Gly			
405	410	415	
Trp Val Leu Gln Glu Pro Ser Ser Glu Leu Cys Leu His Trp Ser Gln			
420	425	430	
Pro Gln Pro Ala Asp Ala Leu Leu Gly Ser Leu Leu Gly Lys Thr Ile			
435	440	445	
Leu Pro Glu Ala Ser Phe Leu Ile Thr Ala Arg Thr Thr Ala Leu Gln			
450	455	460	
Asn Leu Ile Pro Ser Leu Glu Gln Ala Arg Trp Val Glu Val Leu Gly			
465	470	475	480
Phe Ser Glu Ser Ser Arg Lys Glu Tyr Phe Tyr Arg Tyr Phe Thr Asp			
485	490	495	
Glu Arg Gln Ala Ile Arg Ala Phe Arg Leu Val Lys Ser Asn Lys Glu			
500	505	510	
Leu Trp Ala Leu Cys Leu Val Pro Trp Val Ser Trp Leu Ala Cys Thr			
515	520	525	
Cys Leu Met Gln Gln Met Lys Arg Lys Glu Lys Leu Thr Leu Thr Ser			
530	535	540	
Lys Thr Thr Thr Thr Leu Cys Leu His Tyr Leu Ala Gln Ala Leu Gln			
545	550	555	560
Ala Gln Pro Leu Gly Pro Gln Leu Arg Asp Leu Cys Ser Leu Ala Ala			
565	570	575	
Glu Gly Ile Trp Gln Lys Lys Thr Leu Phe Ser Pro Asp Asp Leu Arg			
580	585	590	
Lys His Gly Leu Asp Gly Ala Ile Ile Ser Thr Phe Leu Lys Met Gly			
595	600	605	
Ile Leu Gln Glu His Pro Ile Pro Leu Ser Tyr Ser Phe Ile His Leu			
610	615	620	
Cys Phe Gln Glu Phe Phe Ala Ala Met Ser Tyr Val Leu Glu Asp Glu			
625	630	635	640
Lys Gly Arg Gly Lys His Ser Asn Cys Ile Ile Asp Leu Glu Lys Thr			
645	650	655	
Leu Glu Ala Tyr Gly Ile His Gly Leu Phe Gly Ala Ser Thr Thr Arg			
660	665	670	
Phe Leu Leu Gly Leu Leu Ser Asp Glu Gly Glu Arg Glu Met Glu Asn			
675	680	685	

Ile Phe His Cys Arg Leu Ser Gln Gly Arg Asn Leu Met Gln Trp Val  
 690 695 700  
 Pro Ser Leu Gln Leu Leu Leu Gln Pro His Ser Leu Glu Ser Leu His  
 705 710 715 720  
 Cys Leu Tyr Glu Thr Arg Asn Lys Thr Phe Leu Thr Gln Val Met Ala  
 725 730 735  
 His Phe Glu Glu Met Gly Met Cys Val Glu Thr Asp Met Glu Leu Leu  
 740 745 750  
 Val Cys Thr Phe Cys Ile Lys Phe Ser Arg His Val Lys Lys Leu Gln  
 755 760 765  
 Leu Ile Glu Gly Arg Gln His Arg Ser Thr Trp Ser Pro Thr Met Val  
 770 775 780  
 Val Leu Phe Arg Trp Val Pro Val Thr Asp Ala Tyr Trp Gln Ile Leu  
 785 790 795 800  
 Phe Ser Val Leu Lys Val Thr Arg Asn Leu Lys Glu Leu Asp Leu Ser  
 805 810 815  
 Gly Asn Ser Leu Ser His Ser Ala Val Lys Ser Leu Cys Lys Thr Leu  
 820 825 830  
 Arg Arg Pro Arg Cys Leu Leu Glu Thr Leu Arg Leu Ala Gly Cys Gly  
 835 840 845  
 Leu Thr Ala Glu Asp Cys Lys Asp Leu Ala Phe Gly Leu Arg Ala Asn  
 850 855 860  
 Gln Thr Leu Thr Glu Leu Asp Leu Ser Phe Asn Val Leu Thr Asp Ala  
 865 870 875 880  
 Gly Ala Lys His Leu Cys Gln Arg Leu Arg Gln Pro Ser Cys Lys Leu  
 885 890 895  
 Gln Arg Leu Gln Leu Val Ser Cys Gly Leu Thr Ser Asp Cys Cys Gln  
 900 905 910  
 Asp Leu Ala Ser Val Leu Ser Ala Ser Pro Ser Leu Lys Glu Leu Asp  
 915 920 925  
 Leu Gln Gln Asn Asn Leu Asp Asp Val Gly Val Arg Leu Leu Cys Glu  
 930 935 940  
 Gly Leu Arg His Pro Ala Cys Lys Leu Ile Arg Leu Gly Leu Asp Gln  
 945 950 955 960  
 Thr Thr Leu Ser Asp Glu Met Arg Gln Glu Leu Arg Ala Leu Glu Gln  
 965 970 975  
 Glu Lys Pro Gln Leu Leu Ile Phe Ser Arg Arg Lys Pro Ser Val Met  
 980 985 990  
 Thr Pro Thr Glu Gly Leu Asp Thr Gly Glu Met Ser Asn Ser Thr Ser  
 995 1000 1005  
 Ser Leu Lys Arg Gln Arg Leu Gly Ser Glu Arg Ala Ala Ser His Val  
 1010 1015 1020  
 Ala Gln Ala Asn Leu Lys Leu Leu Asp Val Ser Lys Ile Phe Pro Ile  
 1025 1030 1035 1040  
 Ala Glu Ile Ala Glu Glu Ser Ser Pro Glu Val Val Pro Val Glu Leu  
 1045 1050 1055  
 Leu Cys Val Pro Ser Pro Ala Ser Gln Gly Asp Leu His Thr Lys Pro  
 1060 1065 1070  
 Leu Gly Thr Asp Asp Phe Trp Gly Pro Thr Gly Pro Val Ala Thr  
 1075 1080 1085  
 Glu Val Val Asp Lys Glu Lys Asn Leu Tyr Arg Val His Phe Pro Val  
 1090 1095 1100  
 Ala Gly Ser Tyr Arg Trp Pro Asn Thr Gly Leu Cys Phe Val Met Arg  
 1105 1110 1115 1120  
 Glu Ala Val Thr Val Glu Ile Glu Phe Cys Val Trp Asp Gln Phe Leu  
 1125 1130 1135  
 Gly Glu Ile Asn Pro Gln His Ser Trp Met Val Ala Gly Pro Leu Leu

	1140	1145	1150
Asp Ile Lys Ala Glu Pro Gly Ala Val Glu Ala Val His Leu Pro His			
1155	1160	1165	
Phe Val Ala Leu Gln Gly Gly His Val Asp Thr Ser Leu Phe Gln Met			
1170	1175	1180	
Ala His Phe Lys Glu Glu Gly Met Leu Leu Glu Lys Pro Ala Arg Val			
1185	1190	1195	1200
Glu Leu His His Ile Val Leu Glu Asn Pro Ser Phe Ser Pro Leu Gly			
1205	1210	1215	
Val Leu Leu Lys Met Ile His Asn Ala Leu Arg Phe Ile Pro Val Thr			
1220	1225	1230	
Ser Val Val Leu Tyr His Arg Val His Pro Glu Glu Val Thr Phe			
1235	1240	1245	
His Leu Tyr Leu Ile Pro Ser Asp Cys Ser Ile Arg Lys Glu Leu Glu			
1250	1255	1260	
Leu Cys Tyr Arg Ser Pro Gly Glu Asp Gln Leu Phe Ser Glu Phe Tyr			
1265	1270	1275	1280
Val Gly His Leu Gly Ser Gly Ile Arg Leu Gln Val Lys Asp Lys Lys			
1285	1290	1295	
Asp Glu Thr Leu Val Trp Glu Ala Leu Val Lys Pro Gly Asp Leu Met			
1300	1305	1310	
Pro Ala Thr Thr Leu Ile Pro Pro Ala Arg Ile Ala Val Pro Ser Pro			
1315	1320	1325	
Leu Asp Ala Pro Gln Leu Leu His Phe Val Asp Gln Tyr Arg Glu Gln			
1330	1335	1340	
Leu Ile Ala Arg Val Thr Ser Val Glu Val Val Leu Asp Lys Leu His			
1345	1350	1355	1360
Gly Gln Val Leu Ser Gln Glu Gln Tyr Glu Arg Val Leu Ala Glu Asn			
1365	1370	1375	
Thr Arg Pro Ser Gln Met Arg Lys Leu Phe Ser Leu Ser Gln Ser Trp			
1380	1385	1390	
Asp Arg Lys Cys Lys Asp Gly Leu Tyr Gln Ala Leu Lys Glu Thr His			
1395	1400	1405	
Pro His Leu Ile Met Glu Leu Trp Glu Lys Gly Ser Lys Lys Gly Leu			
1410	1415	1420	
Leu Pro Leu Ser Ser			
1425			

<210> 3  
<211> 5059  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (314)...(1606)

<400> 3

ctgggttctca	acttttttg	aaataatgtt	catagagaag	gagggtgtc	tgagattcga	60
gggaaacaag	ctctcaggac	ttccggtcgc	catgtggct	gtggcggtta	aacgcggta	120
gtgcaagcat	ctggccatc	ttcaatggta	aaaaagatac	agtaaaagaca	taaataccac	180
atttgacaaa	tggaaaaaaa	ggagtgtcca	gaaaagagta	gcagcagtga	ggaagagctg	240
ccgagacggg	tatacaggg	gctaccctgt	gtttctgaga	ccctttgtga	catctcacat	300
tttttccaag	aag atg	atg aga	cag agg	cag agc	cat tat tgt	349
					Met Met Arg Gln Arg Gln Ser His Tyr Cys Ser Val	
	1	5	10			

ctg ttc ctg agt gtc aac tat ctg ggg ggg aca ttc cca gga gac att Leu Phe Leu Ser Val Asn Tyr Leu Gly Gly Thr Phe Pro Gly Asp Ile 15                   20                   25	397
tgc tca gaa gag aat caa ata gtt tcc tct tat gct tct aaa gtc tgt Cys Ser Glu Glu Asn Gln Ile Val Ser Ser Tyr Ala Ser Lys Val Cys 30                   35                   40	445
ttt gag atc gaa gaa gat tat aaa aat cgt cag ttt ctg ggg cct gaa Phe Glu Ile Glu Glu Asp Tyr Lys Asn Arg Gln Phe Leu Gly Pro Glu 45                   50                   55                   60	493
gga aat gtg gat gtt gag ttg att gat aag agc aca aac aga tac agc Gly Asn Val Asp Val Glu Leu Ile Asp Lys Ser Thr Asn Arg Tyr Ser 65                   70                   75	541
gtt tgg ttc ccc act gct ggc tgg tat ctg tgg tca gcc aca ggc ctc Val Trp Phe Pro Thr Ala Gly Trp Tyr Leu Trp Ser Ala Thr Gly Leu 80                   85                   90	589
ggc ttc ctg gta agg gat gag gtc aca gtg acg att gcg ttt ggt tcc Gly Phe Leu Val Arg Asp Glu Val Thr Val Thr Ile Ala Phe Gly Ser 95                   100                  105	637
tgg agt cag cac ctg gcc ctg gac ctg cag cac cat gaa cag tgg ctg Trp Ser Gln His Leu Ala Leu Asp Leu Gln His His Glu Gln Trp Leu 110                 115                 120	685
gtg ggc ggc ccc ttg ttt gat gtc act gca gag cca gag gag gct gtc Val Gly Gly Pro Leu Phe Asp Val Thr Ala Glu Pro Glu Glu Ala Val 125                 130                 135                 140	733
gcc gaa atc cac ctc ccc cac ttc atc tcc ctc caa ggt gag gtg gac Ala Glu Ile His Leu Pro His Phe Ile Ser Leu Gln Gly Glu Val Asp 145                 150                 155	781
gtc tcc tgg ttt ctc gtt gcc cat ttt aag aat gaa ggg atg gtc ctg Val Ser Trp Phe Leu Val Ala His Phe Lys Asn Glu Gly Met Val Leu 160                 165                 170	829
gag cat cca gcc cggtg gag cct ttc tat gct gtc ctg gaa agc ccc Glu His Pro Ala Arg Val Glu Pro Phe Tyr Ala Val Leu Glu Ser Pro 175                 180                 185	877
agc ttc tct ctg atg ggc atc ctg ctg cggtg atc gac ggt act cgc Ser Phe Ser Leu Met Gly Ile Leu Leu Arg Ile Ala Ser Gly Thr Arg 190                 195                 200	925
ctc tcc atc ccc atc act tcc aac aca ttg atc tat tat cac ccc cac Leu Ser Ile Pro Ile Thr Ser Asn Thr Leu Ile Tyr Tyr His Pro His 205                 210                 215                 220	973
ccc gaa gat att aag ttc cac ttg tac ctt gtc ccc agc gac gcc ttg Pro Glu Asp Ile Lys Phe His Leu Tyr Leu Val Pro Ser Asp Ala Leu 225                 230                 235	1021
cta aca aag gcg ata gat gat gag gaa gat cgc ttc cat ggt gtg cgc	1069

Leu Thr Lys Ala Ile Asp Asp Glu Glu Asp Arg Phe His Gly Val Arg			
240	245	250	
ctg cag act tcg ccc cca atg gaa ccc ctg aac ttt ggt tcc agt tat		1117	
Leu Gln Thr Ser Pro Pro Met Glu Pro Leu Asn Phe Gly Ser Ser Tyr			
255	260	265	
att gtg tct aat tct gct aac ctg aaa gta atg ccc aag gag ttg aaa		1165	
Ile Val Ser Asn Ser Ala Asn Leu Lys Val Met Pro Lys Glu Leu Lys			
270	275	280	
ttg tcc tac agg agc cct gga gaa att cag cac ttc tca aaa ttc tat		1213	
Leu Ser Tyr Arg Ser Pro Gly Glu Ile Gln His Phe Ser Lys Phe Tyr			
285	290	295	300
gct ggg cag atg aag gaa ccc att caa ctt gag att act gaa aaa aga		1261	
Ala Gly Gln Met Lys Glu Pro Ile Gln Leu Glu Ile Thr Glu Lys Arg			
305	310	315	
cat ggg act ttg gtg tgg gat act gag gtg aag cca gtg gat ctc cag		1309	
His Gly Thr Leu Val Trp Asp Thr Glu Val Lys Pro Val Asp Leu Gln			
320	325	330	
ctt gta gct gca tca gcc cct cct ttc tca ggt gca gcc ttt gtg		1357	
Leu Val Ala Ala Ser Ala Pro Pro Pro Phe Ser Gly Ala Ala Phe Val			
335	340	345	
aag gag aac cac cggcaa ctc caa gcc agg atg ggg gac ctg aaa ggg		1405	
Lys Glu Asn His Arg Gln Leu Gln Ala Arg Met Gly Asp Leu Lys Gly			
350	355	360	
gtg ctc gat gat ctc cag gac aat gag gtt ctt act gag aat gag aag		1453	
Val Leu Asp Asp Leu Gln Asp Asn Glu Val Leu Thr Glu Asn Glu Lys			
365	370	375	380
gag ctg gtg gag cag gaa aag aca cgg cag agc aag aat gag gcc ttg		1501	
Glu Leu Val Glu Gln Glu Lys Thr Arg Gln Ser Lys Asn Glu Ala Leu			
385	390	395	
ctg agc atg gtg gag aag aaa ggg gac ctg gcc ctg gac gtg ctc ttc		1549	
Leu Ser Met Val Glu Lys Lys Gly Asp Leu Ala Leu Asp Val Leu Phe			
400	405	410	
aga agc att agt gaa agg gac cct tac ctc gtg tcc tat ctt aga cag		1597	
Arg Ser Ile Ser Glu Arg Asp Pro Tyr Leu Val Ser Tyr Leu Arg Gln			
415	420	425	
cag aat ttg taaaatgagt cagtttagta gtctggaaga gagaatccag		1646	
Gln Asn Leu			
430			
cgttctcatt ggaaatggat aaacagaaat gtgatcattt atttcagtgt tcaagacaga		1706	
agaagactgg gtaacatcta tcacacaggc tttcaggaca gacttgtaac ctggcatgta		1766	
cctattgact gtatcctcat gcattttcct caagaatgtc tgaagaagg agtaatattc		1826	
cttttaatt ttttccaacc attgcttgat atatcactat tttatccatt gacatgattc		1886	
ttgaagaccc aggataaagg acatccggat aggtgtgtt atgaaggatg gggcctggaa		1946	
aggcaacttt tcctgattaa tgtaaaaat aattcctatg gacactccgt ttgaagtatc		2006	

acccctctcat	aactaaaaagc	agaaaaagcta	acaaaagctt	ctcagctgag	gacactcaag	2066
gcatacatga	tgacagtctt	ttttttttt	gtatgttagg	actttaacac	tttatctatg	2126
gctactgtta	ttagaacaat	gtaaatgtat	ttgctgaaag	agagcacaaa	aatgggagaa	2186
aatgcaaaca	tgagcagaaaa	atatttccc	actggtgtgt	agcctgtac	aaggagttgt	2246
tgggttaaat	gttcatggtc	aactccaagg	aatactgaga	tgaaatgtgg	taaatcaact	2306
ccacagaacc	acccaaaaga	aatgagggt	aattcagctt	attctgagac	agacattcct	2366
ggcaatgtac	cataaaaaaa	ataagccaac	tctgacattt	ggattctacc	atagactctg	2426
tcatTTTGA	gcacatttcag	ctgtctttt	attaatgttt	tcgtggaca	catatttcca	2486
tcctttatg	ttaatctgt	ttaaaaacaag	ttcctagtag	acaccatctg	gtttagttag	2546
tttttttat	ggtgtatTTT	gaacccattc	tgatagtctc	tttaactgg	aagatttcaa	2606
ttacttacgt	taatgttaatt	attaatatgt	taggatttat	cctcagtcag	ccagtttgg	2666
atgtctttc	tattctactg	ttatcacatt	tgtaccactt	aaagtggaaat	ctaggcactt	2726
tatcaccatt	tagatccatat	tacctttct	cac taggat	atagttatct	tctacataat	2786
ctttctgtat	cttaaaaaccc	atcaataaaat	tattatataat	tttctacttt	taatcactca	2846
gaagatttaa	aaaactcatg	agaagagtaa	tctgttatgt	tttccagat	atttaccatt	2906
tctgttgctc	ttccttcatt	atttccaaa	tttcgttctg	caaatttcca	cttcttctga	2966
tagacgttt	ttagttctt	tagagtggtt	ctgataggtt	cagattctct	tatTTTTC	3026
ttcctctgag	gacatcttt	tctcaccttc	attctcagtg	atgtttttt	ctttagttagt	3086
tttaggttga	cattgtttc	tgttcagcag	tttcccttta	gcttccgtat	ttctgtatga	3146
gaaatctgca	gtcattcaaa	ttgttggttt	cctgtatgtt	gtgtgtcatt	tttctgtcag	3206
atttcaaggt	atttatcttt	agtttttagc	catttcattt	tgttggggat	gagtttcctt	3266
gttttattcc	cttggaaatt	tgctccaatt	cataaatttg	cagttttatg	tcttttacca	3326
aacttagagg	tttcagcct	aatttctaaa	aatactttt	attagcctga	ttttcatctt	3386
tataggaat	agtttaagtg	atgacaagtt	ccaatagctt	atatgccag	aaggccttca	3446
aaataagaat	tttggaaagaa	tacagaaaaac	aaacttttat	atccttctca	tgtcttctac	3506
tgtaaaattc	atatgtttt	ctactctaaa	cctagtttga	aatcaacagt	ctttagaata	3566
gatgaaaatt	ttgatgaata	gttggaaattct	ttttaatgg	aacctcttac	atgtgatttt	3626
ccttgccatc	tagaaataaa	ccatagttt	tatgttgaat	caatcaat	tatTTTGT	3686
ttttttcctc	ctcttctgag	actcttattt	ttggaaatgtt	agacttttat	gtttccttta	3746
atgtccctga	tattctactt	atttagaaaca	tcttttcattt	tttccattt	ttctgattgg	3806
gtaattttaa	tttgtctatt	ttcaaaattt	ctggagttt	cacctgtt	tgtctgtgtc	3866
gtcccactga	gtgcattcac	cacctttaa	attttggtca	ctgtatgtat	cagttctaaa	3926
atttccattt	tgttctctat	atttaaattt	tcttggctta	tattctattt	tcctgcaaat	3986
gtgtcagcat	ttgttggttt	gagttttttt	tttttcaaga	cagggtctca	actctgttac	4046
ccaggctgga	gtgcagttgt	gcgatctcag	ctcaactgcaa	cctctgcctc	ctggttcaag	4106
cgattattgt	gcctcagcct	cctgagtagc	tggattaca	ggcatgcacc	accacagccc	4166
agctaatttt	ttgttattttt	agtagagaca	gagttttgt	atgttggcca	ggctgggtt	4226
gaactccgg	cctcaagtga	tccaccacc	tcagcctccc	aaagtgcgg	gattacaggc	4286
cactacaccc	ggcacattt	agtattttttt	ttttttttt	tttttgaga	tggagtctcg	4346
ctctgtcattc	tagctggag	tcagttgtt	tgatctcagc	tcactgcagc	ctctgtctcc	4406
cgggctcaag	cgattcttt	gcctcagcct	cctgagtagc	taggactaca	ggtgcattcc	4466
aacacgccc	gctaattttt	ttaaaaaata	tttttagtag	agacagggtt	tcaccattt	4526
ggccaggatg	gtctcgatct	cctgacccca	tgatccaccc	gcctcggct	tccaaagtgc	4586
tgggattaca	ggcatgagcc	accgtgcct	gcctcatttt	agtattttta	taatgtctct	4646
tttaaagtct	ttgtcagata	attccactgt	acatgttatt	cagtgtttgg	tgtccactga	4706
gttgtcattt	gccagacaag	tggagatttt	tgcaagctcat	ccttgttattc	tcagtagttc	4766
cgatatgtac	cctcgacatg	tgaatgttat	cttatgagac	tctgttttat	ttgtatccaa	4826
cagaagatgt	ttatttattt	tttggcttcc	tgtgaactga	ggtcttaata	tcagctcatt	4886
ttaaaaagtct	ttgcagttgtt	attcggatct	atcctgtgt	tgcctatgag	attgggtgca	4946
gtgtatcctg	ttagctccat	tctcaggcgc	tttgaatgtg	aatttaggacc	agcgaatga	5006
atgctcaagt	tggggttggg	cgttagaatt	cataaaaagtc	tttatatgtct	cag	5059

<210> 4  
<211> 431  
<212> PRT  
<213> *Homo sapiens*

&lt;400&gt; 4

Met	Met	Arg	Gln	Arg	Gln	Ser	His	Tyr	Cys	Ser	Val	Leu	Phe	Leu	Ser
1															15
Val	Asn	Tyr	Leu	Gly	Gly	Thr	Phe	Pro	Gly	Asp	Ile	Cys	Ser	Glu	Glu
															30
Asn	Gln	Ile	Val	Ser	Ser	Tyr	Ala	Ser	Lys	Val	Cys	Phe	Glu	Ile	Glu
															45
Glu	Asp	Tyr	Lys	Asn	Arg	Gln	Phe	Leu	Gly	Pro	Glu	Gly	Asn	Val	Asp
															60
Val	Glu	Leu	Ile	Asp	Lys	Ser	Thr	Asn	Arg	Tyr	Ser	Val	Trp	Phe	Pro
65															80
Thr	Ala	Gly	Trp	Tyr	Leu	Trp	Ser	Ala	Thr	Gly	Leu	Gly	Phe	Leu	Val
															95
Arg	Asp	Glu	Val	Thr	Val	Thr	Ile	Ala	Phe	Gly	Ser	Trp	Ser	Gln	His
															110
Leu	Ala	Leu	Asp	Leu	Gln	His	His	Glu	Gln	Trp	Leu	Val	Gly	Gly	Pro
															125
Leu	Phe	Asp	Val	Thr	Ala	Glu	Pro	Glu	Glu	Ala	Val	Ala	Glu	Ile	His
															140
Leu	Pro	His	Phe	Ile	Ser	Leu	Gln	Gly	Glu	Val	Asp	Val	Ser	Trp	Phe
145															160
Leu	Val	Ala	His	Phe	Lys	Asn	Glu	Gly	Met	Val	Leu	Glu	His	Pro	Ala
															175
Arg	Val	Glu	Pro	Phe	Tyr	Ala	Val	Leu	Glu	Ser	Pro	Ser	Phe	Ser	Leu
															190
Met	Gly	Ile	Leu	Leu	Arg	Ile	Ala	Ser	Gly	Thr	Arg	Leu	Ser	Ile	Pro
															205
Ile	Thr	Ser	Asn	Thr	Leu	Ile	Tyr	Tyr	His	Pro	His	Pro	Glu	Asp	Ile
															220
Lys	Phe	His	Leu	Tyr	Leu	Val	Pro	Ser	Asp	Ala	Leu	Leu	Thr	Lys	Ala
225															240
Ile	Asp	Asp	Glu	Glu	Asp	Arg	Phe	His	Gly	Val	Arg	Leu	Gln	Thr	Ser
															255
Pro	Pro	Met	Glu	Pro	Leu	Asn	Phe	Gly	Ser	Ser	Tyr	Ile	Val	Ser	Asn
															270
Ser	Ala	Asn	Leu	Lys	Val	Met	Pro	Lys	Glu	Leu	Lys	Leu	Ser	Tyr	Arg
															285
Ser	Pro	Gly	Glu	Ile	Gln	His	Phe	Ser	Lys	Phe	Tyr	Ala	Gly	Gln	Met
															300
Lys	Glu	Pro	Ile	Gln	Leu	Glu	Ile	Thr	Glu	Lys	Arg	His	Gly	Thr	Leu
305															320
Val	Trp	Asp	Thr	Glu	Val	Lys	Pro	Val	Asp	Leu	Gln	Leu	Val	Ala	Ala
															335
Ser	Ala	Pro	Pro	Pro	Phe	Ser	Gly	Ala	Ala	Phe	Val	Lys	Glu	Asn	His
															350
Arg	Gln	Leu	Gln	Ala	Arg	Met	Gly	Asp	Leu	Lys	Gly	Val	Leu	Asp	Asp
															365
Leu	Gln	Asp	Asn	Glu	Val	Leu	Thr	Glu	Asn	Glu	Lys	Glu	Leu	Val	Glu
															380
Gln	Glu	Lys	Thr	Arg	Gln	Ser	Lys	Asn	Glu	Ala	Leu	Leu	Ser	Met	Val
385															400
Glu	Lys	Lys	Gly	Asp	Leu	Ala	Leu	Asp	Val	Leu	Phe	Arg	Ser	Ile	Ser
															415
Glu	Arg	Asp	Pro	Tyr	Leu	Val	Ser	Tyr	Leu	Arg	Gln	Gln	Asn	Leu	
															430

&lt;210&gt; 5

<211> 4287  
<212> DNA  
<213> Homo sapiens

<400> 5		
atggctggcg gagcctgggg ccgcctggcc tgttacttgg agttcctgaa	gaaggaggag	60
ctgaaggagt tccagttct gctcgccaat aaagcgcact ccaggagctc	ttcggttag	120
acacccgctc agccagagaa gacgagtggc atggaggtgg cctcgtaacct	ggtgctcag	180
tatggggagc agcgggcctg ggacctagcc ctccataacct	gggagcagat	240
tcactgtcg cccaaagccca ggaaggggca ggccactctc	cctcattccc	300
atgaaacccc acctgggtc tcccagccaa cccacactca	ccgcagtgt	360
atccatgaat tgccggcggg gtgcacccag ggctcagaga	gaagggttt	420
cctgacacat ctggacgcgg ctggagagaa atctctgct	cactcctcta	480
ccaaagctccc cagaccatga gtctccaagc caggagtac	ccaacgcccc	540
gcagtgctgg ggagctgggg atccccac	cagcccagcc	600
gctcctggga cccaaatggcc tctggatgaa acgtcaggaa	tagcacccag	660
gaaagagaga gagagaaaatc agagaaaaggc	aggccccat	720
ccccccacagg cgcacaccag cctacagccc	gggcagcgt	780
gagagcctct gttccacatg gcccggaaa	aatgaggatt	840
ctgctacttc tacaagacc tcacccaga	acccaagatc	900
cctgattatg tggagagaa tcgaggacat	ttaattgaga	960
ggcctggata cccaaagaacc tcgcataatgc	atactgcagg	1020
tcaacactgg ccaggcaggt	gaaggaagcc	1080
ttccagcatg tcttctactt	cagctgcaga	1140
gctgagctca tcggaaaaga tgggacagcc	actccggctc	1200
aggccagac ggctgcttt	catcctcgat	1260
gagccgagtt ctgagctctg	tctgcactgg	1320
ggcagttgc tggggaaaac	tataacttccc	1380
acagctctgc agaacatcat	tccttctttg	1440
ttctctgagt ccagcagggaa	ggaatatttc	1500
attagagcct ttaggttgg	taaatcaaac	1560
tgggtgtcct ggctggcctg	cacttgcctg	1620
acactgactt ccaagaccac	cacaaccctc	1680
gctcagccat tgggacccca	gctcagagac	1740
caaaaaaaga cccttttag	tccagatgac	1800
atctccaccc tcttgaagat	gggtattctt	1860
ttcattcacc tctgtttcca	agagttctt	1920
aagggggagag gtaaacattc	taattgcattc	1980
ggaatacatag gcctgtttgg	ggcatcaacc	2040
gagggggaga gagagatgga	gaacatctt	2100
atgcagtggg tcccgtccct	gcagctgctg	2160
tgccttgtac agactcgaa	caaaacgttc	2220
atgggcatgt gtgtagaaac	agacatggag	2280
agccgccacg tgaagaagct	tcaagctgatt	2340
cccacccatgg tagtcctgtt	cagggtgggtc	2400
ttctccgtcc tcaaggtcac	cagaaacctg	2460
agccactctg cagtgaagag	tctttgttaag	2520
accctgcgg	accctgagac	2580
ctgagagcca accagaccct	gaccgagct	2640
ggagccaaac acctttgcca	gagactgaga	2700
ctggtcagct gtggcctcac	gtctgactgc	2760
agcccccagcc tgaaggagct	agacctgcag	2820
ctgctctgtg aggggcttag	gcattcgtcc	2880
acaactctga gtgtatgagat	gaggcaggaa	2940
ctgctcatct tcagcagacg	gaaaccaagt	3000
ggagagatga gtaatagcac	atcctcactc	3060
gcttcccatgt ttgctcaggc	aaacccat	3120

gctgagattt	cagaggaaag	ctccccagag	gtagtaccgg	tggactctt	gtgcgtgcct	3180
tccctgcct	ctcaagggga	cctgcatacg	aagccttgg	ggactgacga	tgacttctgg	3240
ggccccacgg	ggcctgtggc	tactgaggtt	gttgacaaaag	aaaagaacct	gtaccgagtt	3300
caactccctg	tagctggctc	ctaccgctgg	cccaacacgg	gtctctgcct	tgtgatgaga	3360
gaagcggtga	ccgtttagat	tgaattctgt	gtgtgggacc	agttcctggg	ttagatcaac	3420
ccacagcaca	gctggatggt	gcagggcct	ctgctggaca	tcaaggctga	gcctggagct	3480
gttggaaagctg	tgcacccc	tcactttgtt	gctctccaag	ggggccatgt	ggacacatcc	3540
ctgttccaaa	tggcccaactt	taaagaggag	gggatgctcc	tggagaagcc	agccagggtg	3600
gagctgcattc	acatagttct	gaaaaacccc	agcttctccc	ccttgggagt	cctctgaaa	3660
atgatccata	atgccctgcg	cttcattccc	gtcacctctg	ttgtgttgc	ttaccaccgc	3720
gtccatcctg	aggaagtca	cttccaccc	tacctgatcc	caagtgactg	ctccattcgg	3780
aaggaactgg	agctctgcta	tcgaaggcct	ggagaagacc	agctgttctc	ggagttctac	3840
gttggccact	tggatcagg	gatcaggctg	caagtgaaaag	acaagaaaaga	tgagactctg	3900
gtgtgggagg	ccttggtaa	accaggagat	ctcatgcctg	caactactt	gatccctcca	3960
gcccgcata	ccgtaccc	acctctggat	gccccgcagt	tgctgcactt	tgtggaccag	4020
tatcgagac	agctgatagc	ccgagtgaca	tcgggtggagg	ttgtcttga	caaactgcat	4080
ggacaggtgc	tgagccagga	gcagttacgag	agggtgctgg	ctgagaacac	gaggcccagc	4140
cagatgcgga	agctgttcag	cttgagccag	tccttggacc	gaaagtgc	agatggactc	4200
taccaagccc	tgaaggagac	ccatcctcac	ctcattatgg	aactctggg	gaagggcagc	4260
aaaaagggac	tcctgccact	cagcagc				4287

<210> 6  
<211> 1293  
<212> DNA  
<213> Homo sapiens

<400> 6						
atgatgagac	agaggcagag	ccattattgt	tccgtgttgt	tcctgagtgt	caactatctg	60
ggggggacat	tcccaggaga	catttgc	ca	aaagagaatc	aatagttc	120
tctaaagtct	gttttggat	cgaagaagat	tataaaaatc	gtcagtttct	ggggcctgaa	180
ggaaatgtgg	atgttggat	gattgataag	agcacaaaca	gatacagcgt	ttgggtcccc	240
actgctggct	ggtatctgt	gtcagccaca	ggcctcggct	tccttggta	ggatgagg	300
acagtgc	ttgcgttgg	ttcctggagt	cagcac	ccctggac	gcagcac	360
gaacagtggc	tggtggcgg	ccc	ttt	gatgtca	cagagccaga	420
gccgaaatcc	accc	cc	cc	ctccaa	agg	480
ctcg	ttt	aa	aa	gttggac	gttgg	540
ttctatg	tc	ct	ct	atcc	gg	600
atgggactc	gc	ct	cc	cc	at	660
cccgaaagata	tta	at	tt	cc	cc	720
atagatgat	agg	aa	gg	cc	cc	780
ccc	ct	cc	cc	cc	cc	840
aaggagttg	a	tt	tt	cc	cc	900
gttggcaga	t	g	g	cc	cc	960
gtgtggata	ct	g	g	gg	gg	1020
ccttctc	gt	g	g	cc	cc	1080
gac	gg	gt	gt	cc	cc	1140
gagaagaa	gg	gt	gt	cc	cc	1200
gggac	gg	gt	gt	cc	cc	1260
tac	cc	ta	tt	cc	cc	1293

<210> 7  
<211> 740  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS

<222> (54) . . . (638)

195

atcatcctga atctgatctt tttatacaca atatacgaaa agccagcttg aa 740

&lt;210&gt; 8

&lt;211&gt; 195

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 8

Met	Gly	Arg	Ala	Arg	Asp	Ala	Ile	Leu	Asp	Ala	Leu	Glu	Asn	Leu	Thr	
1							5				10				15	

Ala	Glu	Glu	Leu	Lys	Lys	Phe	Lys	Leu	Lys	Leu	Leu	Ser	Val	Pro	Leu
								20		25				30	

Arg	Glu	Gly	Tyr	Gly	Arg	Ile	Pro	Arg	Gly	Ala	Leu	Leu	Ser	Met	Asp
							35		40				45		

Ala	Leu	Asp	Leu	Thr	Asp	Lys	Leu	Val	Ser	Phe	Tyr	Leu	Glu	Thr	Tyr
							50		55			60			

Gly	Ala	Glu	Leu	Thr	Ala	Asn	Val	Leu	Arg	Asp	Met	Gly	Leu	Gln	Glu
65							70				75			80	

Met	Ala	Gly	Gln	Leu	Gln	Ala	Ala	Thr	His	Gln	Gly	Ser	Gly	Ala	Ala
							85			90			95		

Pro	Ala	Gly	Ile	Gln	Ala	Pro	Pro	Gln	Ser	Ala	Ala	Lys	Pro	Gly	Leu
							100		105			110			

His	Phe	Ile	Asp	Gln	His	Arg	Ala	Ala	Leu	Ile	Ala	Arg	Val	Thr	Asn
							115		120			125			

Val	Glu	Trp	Leu	Leu	Asp	Ala	Leu	Tyr	Gly	Lys	Val	Leu	Thr	Asp	Glu
							130		135			140			

Gln	Tyr	Gln	Ala	Val	Arg	Ala	Glu	Pro	Thr	Asn	Pro	Ser	Lys	Met	Arg
145							150			155			160		

Lys	Leu	Phe	Ser	Phe	Thr	Pro	Ala	Trp	Asn	Trp	Thr	Cys	Lys	Asp	Leu
							165			170			175		

Leu	Leu	Gln	Ala	Leu	Arg	Glu	Ser	Gln	Ser	Tyr	Leu	Val	Glu	Asp	Leu
							180		185			190			

Glu	Arg	Ser													
		195													

&lt;210&gt; 9

&lt;211&gt; 585

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 9

atggggcgcg	cgcgcgacgc	catcctggat	gcgctggaga	acctgaccgc	cgaggagctc	60
aagaagtta	agctgaagct	gctgtcggt	ccgctgcgcg	agggctacgg	gcccacatccc	120
ccccggcg	tgctgtccat	gacgccttg	gacccatcccg	acaagctgt	cagcttctac	180
ctggagac	acggccgcga	gctcaccgct	aacgtgtgc	gcgcacatggg	cctgcaggag	240
atggccgg	agctgcaggc	gcccacgcac	cagggtcttg	gagccgcgc	agctgggatc	300
caggcc	tcagtcggc	agccaagcca	ggcctgcact	ttatagacca	gcaccgggct	360
gcgttat	cgagggtcac	aaacgttgag	tggctgtgg	atgctctgt	cgggaaggtc	420
ctgacggat	agcagtagcca	ggcagtgcgg	gcccggccca	ccaacccaag	caagatgcgg	480
aagcttca	gtttcacacc	agcctggaaac	tggacctgca	aggacttgct	cctccaggcc	540
ctaaggag	cccagtccta	cctggggag	gacctggagc	ggagc		585

&lt;210&gt; 10

&lt;211&gt; 740

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 10

ttcaagctgg	ctttcgtat	attgtgtata	aaaagatcat	attcaggatg	atttgggtgg	60
attgccagg	gctgaccgga	gtgttgcgtgg	gaaggaggcct	cagctccgct	ccaggtcctc	120
caccaggtag	gactgggact	cccttagggc	ctggaggagc	aagtccctgc	aggtccagg	180
ccaggctgg	gtgaaactga	agagcttcgg	catctgcgtt	gggttgggtgg	gctcgccccg	240
cactgcctgg	tactgctcat	ccgtcaggac	cttcccgta	agagcatcca	gcagccactc	300
aacgtttgt	accctcgcg	taagcgcagc	ccgggtgtgg	tctataaaagt	gcaggcctgg	360
cttggctgcc	gactgaggag	gggcctggat	cccagctggc	gcggctccag	agccctggtg	420
cgtggccgccc	tgcagctgcc	cggccatctc	ctgcaggccc	atgtcgcgca	gcacgttagc	480
gttgagctcg	gcgcgttagg	tctccaggtt	gaagctgacc	agcttgcgtgg	tgagggtccaa	540
ggcgtccatg	gacagcagcg	ccccccgggg	gatgcgcgg	tagccctcg	gcagcggcac	600
cgacagcagc	ttcagcttga	acttctttag	ctcctcgccg	gtcagggttct	ccagcgcata	660
caggatggcg	tcgcgcgcgc	ccccatggc	tccaggatcc	ccggccgctg	ccgcccgtca	720
ccccgctgca	gccggacgcg					740